Amendment to the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Drawings.

Please amend the paragraph beginning at page 11, line 13, as follows:

Fig. 1A: Profile of the PSGL-1 19ek peptides resolved by anion-exchange chromatography. See text for definition of peak labels. Inset. Structure of the major PSGL-1 19ek peptide SGP-3. <Q denotes cyclization of the N-terminal Gln residue to pyroglutamate and SO_3 represents sulfation of Tyr residues. The over line in the numbered peptide sequence (SEQ ID NO:5) indicates residues of non-PSGL-1 origin that are associated with the enterokinase linker region.

Please amend the paragraph beginning at page 13, line 19, as follows:

Figures 6A, 6B and 6C provide the amino acid sequences of P-selectin (SEQ ID NO:1) (Fig. 6A), E-selectin (SEQ ID NO:2) (Fig. 6B) and PSGL-1 (SEQ ID NO:3) (Fig. 6C). The segments of the sequences used to make the constructs in the crystals are underlined.

Please amend the paragraph beginning at page 29, line 24, as follows:

Generation of Constructs and Protein/Peptide Preparation. The lectin-EGF (LE) domains (153 amino acids) of P-selectin (P-LE) and E-selectin (E-LE) fused to the CH2-CH3 region of IgG_1 via an intervening enterokinase cleavage sequence (Asp-Asp-Asp-Asp-Lys (SEQ ID NO:4)) were expressed in CHO cells and recovered from conditioned media by protein A sepharose (Pharmacia) chromatography. Monomeric selectin LE domains were produced by digestion of the dimeric Fc constructs with enterokinase (LaVallie et al., 1993) and the enzyme and residual Fc domains were removed by chromatography over tandem soy bean trypsin inhibitor-agarose (Sigma) and protein A (Perseptive Biosystems) columns. The selectin LE domains were deglycosylated at 37° C for 48 hrs at a ratio of 25 milliunits N-glycanase/mg protein and purified by anion exchange and hydrophobic interaction chromatography. LE domains were brought to 10-30 mg/ml by vacuum concentration. Both P-LE and E-LE were

determined to be correct by mass spectrometry (MS), monomeric by gel filtration HPLC, and functional by surface plasmon resonance (BIAcore) analysis (see below).